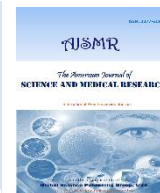




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Review Article

Bioprospecting of Microorganisms for Novel Enzymatic Degradation of Pollutants

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ABSTRACT

Environmental pollution caused by persistent organic and inorganic contaminants has become a major global challenge, threatening ecosystem stability, biodiversity, and human health. Pollutants such as petroleum hydrocarbons, pesticides, dyes, pharmaceuticals, plastics, and heavy metals are often resistant to natural degradation and may accumulate in soil, water, and sediments for prolonged periods. Conventional physicochemical remediation approaches, including adsorption, incineration, membrane filtration, and chemical oxidation, are frequently associated with high operational costs, energy demand, incomplete treatment efficiency, and secondary waste generation. Consequently, sustainable biological alternatives have gained increasing scientific and industrial attention. Among these, microbial bioprospecting, defined as the systematic exploration of microbial diversity for valuable genes, metabolites, and enzymes, offers a promising route for discovering novel biodegradation systems. Microorganisms inhabiting contaminated soils, wastewater treatment plants, marine ecosystems, landfill sites, industrial effluents, and extreme environments possess unique adaptive metabolisms and robust catalytic machinery for pollutant transformation. Novel enzymes such as laccases, peroxidases, monooxygenases, dioxygenases, hydrolases, dehalogenases, and polyester depolymerases have demonstrated strong potential for degrading a wide range of recalcitrant contaminants into less toxic or reusable products. Recent advances in metagenomics, genomics, transcriptomics, proteomics, artificial intelligence, and synthetic biology have significantly accelerated access to uncultivable microorganisms and previously hidden catabolic pathways, enabling improved enzyme discovery, optimization, and large-scale production. However, challenges related to enzyme stability, substrate specificity, biosafety, regulatory approval, and field-scale implementation remain important constraints. This review critically discusses the ecological significance of environmental pollutants, major sources of pollutant-degrading microorganisms, key enzymatic systems, modern molecular discovery tools, current bioremediation applications, associated limitations, and future prospects for integrating microbial bioprospecting into sustainable environmental management and circular bioeconomy strategies.

1. Introduction

Environmental pollution has become one of the most serious global concerns of the twenty-first century, primarily driven by rapid industrialization, urbanization, agricultural intensification, and unsustainable resource consumption. The continuous discharge of hazardous contaminants into terrestrial and aquatic ecosystems has resulted in severe ecological imbalances and substantial threats to public health.

Pollutants such as petroleum hydrocarbons, pesticides, synthetic dyes, pharmaceuticals, plastics, and heavy metals persist in the environment for prolonged periods because of their chemical stability and resistance to natural degradation processes (Kumar et al., 2021). Their accumulation in soil, water, and sediments may alter ecosystem functioning, reduce biodiversity, and cause toxic effects in plants, animals, and humans.

Conventional remediation strategies, including adsorption, chemical oxidation, membrane filtration,

incineration, and landfilling, have long been employed to manage contaminated environments. Although these methods can be effective under controlled conditions, they often involve high operational costs, extensive energy requirements, incomplete contaminant removal, and the formation of toxic secondary residues (Saravanan et al., 2022). In addition, large-scale implementation of these technologies remains difficult in economically constrained regions. Consequently, the need for cost-effective and environmentally sustainable remediation alternatives has intensified worldwide.

Bioremediation has emerged as a promising solution because it relies on living organisms or their biochemical systems to transform toxic contaminants into less harmful substances. Among biological agents, microorganisms are particularly important due to their vast metabolic diversity, rapid adaptation, and ability to colonize polluted habitats. Bacteria, fungi, archaea, and microalgae possess specialized enzymatic pathways capable of degrading or transforming complex xenobiotic compounds into simpler molecules such as carbon dioxide, water, and biomass (Bhatt et al., 2021). These microbial processes are generally safer and more eco-friendly than physicochemical treatments. The growing demand for efficient biodegradation systems has accelerated interest in microbial bioprospecting. Bioprospecting refers to the systematic exploration of biodiversity for organisms, genes, metabolites, or enzymes with valuable industrial or environmental applications. Polluted soils, wastewater treatment plants, industrial effluents, marine sediments, landfill sites, and extreme environments often harbor microorganisms that have evolved adaptive catabolic mechanisms in response to toxic stress. Such environments represent rich reservoirs of novel enzymes with enhanced tolerance to pH, salinity, temperature, and contaminant load.

Several enzymes identified through microbial bioprospecting, including laccases, peroxidases, monooxygenases, dioxygenases, hydrolases, and depolymerases, have shown considerable potential in degrading recalcitrant pollutants such as dyes, hydrocarbons, pesticides, antibiotics, and synthetic polymers. Recent advances in metagenomics, genomics, transcriptomics, and artificial intelligence-based screening tools have further expanded the discovery of uncultivable microorganisms and previously unknown catabolic genes (Ali et al., 2021). These innovations are enabling the development of next-generation enzymatic technologies for environmental cleanup. Despite significant progress, challenges such as low enzyme stability under field conditions, limited substrate specificity, process scalability, and regulatory constraints still hinder practical application. Therefore, continuous exploration of microbial diversity combined with molecular engineering approaches is essential to improve bioremediation efficiency.

This review critically examines the role of microbial bioprospecting in discovering novel enzymes for pollutant degradation. It discusses major pollutant classes, ecological sources of degradative microorganisms, important enzyme systems, advanced discovery tools, practical bioremediation applications, and future prospects for sustainable environmental management.

1. Environmental Pollutants and Their Ecological Impact

Environmental pollutants are substances introduced into natural ecosystems at concentrations that adversely affect living

organisms, ecological processes, and environmental quality. Rapid industrial growth, expanding urban populations, intensified agriculture, and unsustainable waste disposal practices have substantially increased the release of contaminants into soil, water, and the atmosphere. Many of these pollutants persist for extended periods, undergo long-range transport, and accumulate within food webs, thereby creating chronic ecological and human health risks (Wang et al., 2023). Their effects are often complex because pollutants may interact synergistically, producing toxicity greater than that of individual compounds.

Organic pollutants constitute one of the most widespread categories of environmental contaminants. These include petroleum hydrocarbons, pesticides, polycyclic aromatic hydrocarbons (PAHs), synthetic dyes, chlorinated solvents, pharmaceuticals, and surfactants. Many organic compounds are resistant to degradation because of aromatic rings, halogen substitutions, or high molecular stability. Once released into the environment, they can contaminate groundwater, inhibit microbial diversity, impair plant growth, and exert mutagenic or carcinogenic effects on animals and humans (Zhang et al., 2024). Industrial dyes discharged from textile and leather industries are particularly problematic because they reduce light penetration in aquatic systems, interfere with photosynthesis, and generate toxic breakdown intermediates.

Inorganic pollutants also represent a major ecological threat. Heavy metals such as cadmium, mercury, chromium, arsenic, lead, and nickel are non-biodegradable and remain in ecosystems for long durations. Unlike many organic compounds, metals cannot be mineralized and therefore accumulate in sediments, soils, and biological tissues. Chronic exposure to heavy metals can disrupt enzyme systems, induce oxidative stress, damage cellular membranes, and impair neurological, renal, and reproductive functions in humans and wildlife (Tchounwou et al., 2012; Li et al., 2022). Agricultural soils irrigated with industrial wastewater are particularly vulnerable to metal accumulation, which can subsequently enter crops and the human food chain.

Emerging pollutants have received increasing scientific attention during the last decade. These contaminants include microplastics, nanoplastics, personal care products, endocrine-disrupting chemicals, flame retardants, antibiotics, and pharmaceutical residues. Although often detected at relatively low concentrations, their continuous release and pseudo-persistent nature make them environmentally significant. Antibiotics and pharmaceutical compounds in wastewater treatment effluents may contribute to antimicrobial resistance and alter aquatic microbial communities (Gao et al., 2023). Microplastics can adsorb toxic chemicals, act as vectors for pathogens, and be ingested by aquatic organisms, leading to physical and biochemical stress.

The ecological impacts of pollution extend beyond direct toxicity. Pollutants can modify nutrient cycling, suppress beneficial microbial communities, reduce primary productivity, and destabilize trophic interactions. In aquatic environments, contaminant-induced eutrophication and oxygen depletion may cause fish mortality and biodiversity loss. In soils, persistent pollutants can reduce fertility by affecting microbial-mediated processes such as nitrogen fixation, organic matter decomposition, and phosphorus solubilization. These disturbances ultimately compromise ecosystem resilience and the capacity of natural systems to recover from environmental stress (Singh et al., 2024).

Because environmental pollutants differ widely in chemical structure, mobility, persistence, and toxicity, no single remediation strategy is universally effective. Understanding pollutant classes and their ecological consequences is therefore essential for designing targeted bioremediation systems. Microbial bioprospecting becomes particularly relevant in this context, as diverse contaminated habitats may contain microorganisms naturally adapted to detoxify specific classes of pollutants through novel enzymatic pathways.

2. Microbial Bioprospecting: Concepts and Sources

Microbial bioprospecting refers to the systematic exploration of microbial diversity for the discovery of valuable biological resources such as novel enzymes, metabolites, genes, and biochemical pathways with environmental, industrial, agricultural, or pharmaceutical applications. In the context of pollutant remediation, microbial bioprospecting has become increasingly significant because microorganisms possess extraordinary metabolic flexibility that enables them to survive and function in contaminated environments. Through long-term exposure to toxic compounds, many microbial communities develop adaptive mechanisms that include detoxification pathways, efflux systems, stress-response proteins, and specialized catabolic enzymes capable of degrading otherwise persistent pollutants (Mulligan, 2021; Bhatt et al., 2021). These natural adaptations make microorganisms an exceptional reservoir for identifying new biodegradative systems.

One of the major strengths of microbial bioprospecting lies in the immense and largely unexplored diversity of microorganisms present across global ecosystems. It is estimated that only a small fraction of microbial species has been successfully cultured and characterized under laboratory conditions, while the majority remain uncultivable using conventional techniques. This hidden microbial diversity likely contains a vast number of unknown enzymes with unique catalytic properties such as thermostability, halotolerance, pH tolerance, solvent resistance, and broad substrate specificity (Steen et al., 2019; Almeida et al., 2023). Modern bioprospecting strategies therefore combine ecological sampling with molecular tools to access both culturable and unculturable microbial resources.

Contaminated soils are among the most productive sources for isolating pollutant-degrading microorganisms. Agricultural lands exposed to pesticides, oil-contaminated sites, mining regions, and landfill soils often harbor bacteria and fungi capable of utilizing toxic compounds as carbon or energy sources. Species belonging to genera such as *Pseudomonas*, *Bacillus*, *Rhodococcus*, *Aspergillus*, and *Penicillium* have frequently been associated with hydrocarbon degradation, pesticide transformation, and dye decolorization (Varjani et al., 2020; Bhatt et al., 2021). Because these habitats impose strong chemical selection pressure, resident microbes often evolve enhanced catabolic efficiency.

Aquatic environments also provide valuable opportunities for microbial bioprospecting. Wastewater treatment plants, industrial effluents, river sediments, estuaries, and marine ecosystems receive diverse mixtures of contaminants including pharmaceuticals, detergents, hydrocarbons, and heavy metals. Microorganisms in these systems often exist as complex biofilms or consortia capable of cooperative pollutant degradation. Marine microbes are especially attractive because

they may produce salt-tolerant and pressure-resistant enzymes suitable for industrial applications under harsh conditions (Trincon, 2022). Sediment-associated bacteria and fungi have shown particular promise in degrading aromatic hydrocarbons and synthetic chemicals.

Extreme environments have emerged as frontier targets for discovering robust enzymes. Hot springs, hypersaline lakes, acidic mines, polar regions, and alkaline habitats contain extremophilic microorganisms adapted to severe physicochemical stress. These organisms produce extremozymes that remain active under high temperature, salinity, pH, or metal concentrations, making them highly desirable for pollutant treatment processes where conventional enzymes rapidly lose activity (Coker, Bowers, & Shams, 2022). Enzymes from thermophiles and halophiles are especially relevant for treating industrial effluents generated under non-neutral conditions.

Traditional microbial bioprospecting relied heavily on culture-dependent isolation, enrichment techniques, and biochemical screening. Although still valuable, these methods recover only a limited proportion of environmental microbes. Culture-independent approaches such as metagenomics, amplicon sequencing, single-cell genomics, and functional gene screening now allow researchers to identify catabolic genes directly from environmental DNA without cultivation (Simon & Daniel, 2019; Chistoserdova, 2023). These technologies have accelerated the discovery of novel oxygenases, hydrolases, oxidoreductases, and plastic-degrading enzymes from previously inaccessible microbial communities (Jumper et al., 2021).

The success of microbial bioprospecting depends not only on discovering new organisms but also on understanding ecological interactions within microbial consortia. Many pollutants are too complex to be completely degraded by a single species and instead require sequential or cooperative metabolism among multiple microorganisms. Therefore, future bioprospecting strategies increasingly focus on community-level functions, synthetic consortia design, and systems biology approaches to maximize biodegradation efficiency.

Overall, microbial bioprospecting provides a powerful foundation for identifying next-generation enzymes and microbial systems for sustainable pollutant management. By exploring diverse and extreme habitats through advanced molecular technologies, researchers can significantly expand the toolkit available for environmental bioremediation.

3. Novel Enzymes Involved In Pollutant Degradation

Microbial enzymes are the primary catalytic agents responsible for the biodegradation and detoxification of environmental pollutants. These biocatalysts enable microorganisms to utilize complex contaminants as sources of carbon, nitrogen, phosphorus, or energy, thereby transforming hazardous compounds into less toxic or more biodegradable intermediates. Compared with conventional chemical treatments, enzymatic degradation is highly specific, energy efficient, and environmentally benign. Continuous microbial adaptation in polluted habitats has led to the evolution of novel enzymes with broader substrate ranges, improved catalytic efficiency, and greater tolerance to extreme environmental conditions (Bilal et al., 2022; Sharma et al., 2023). Consequently,

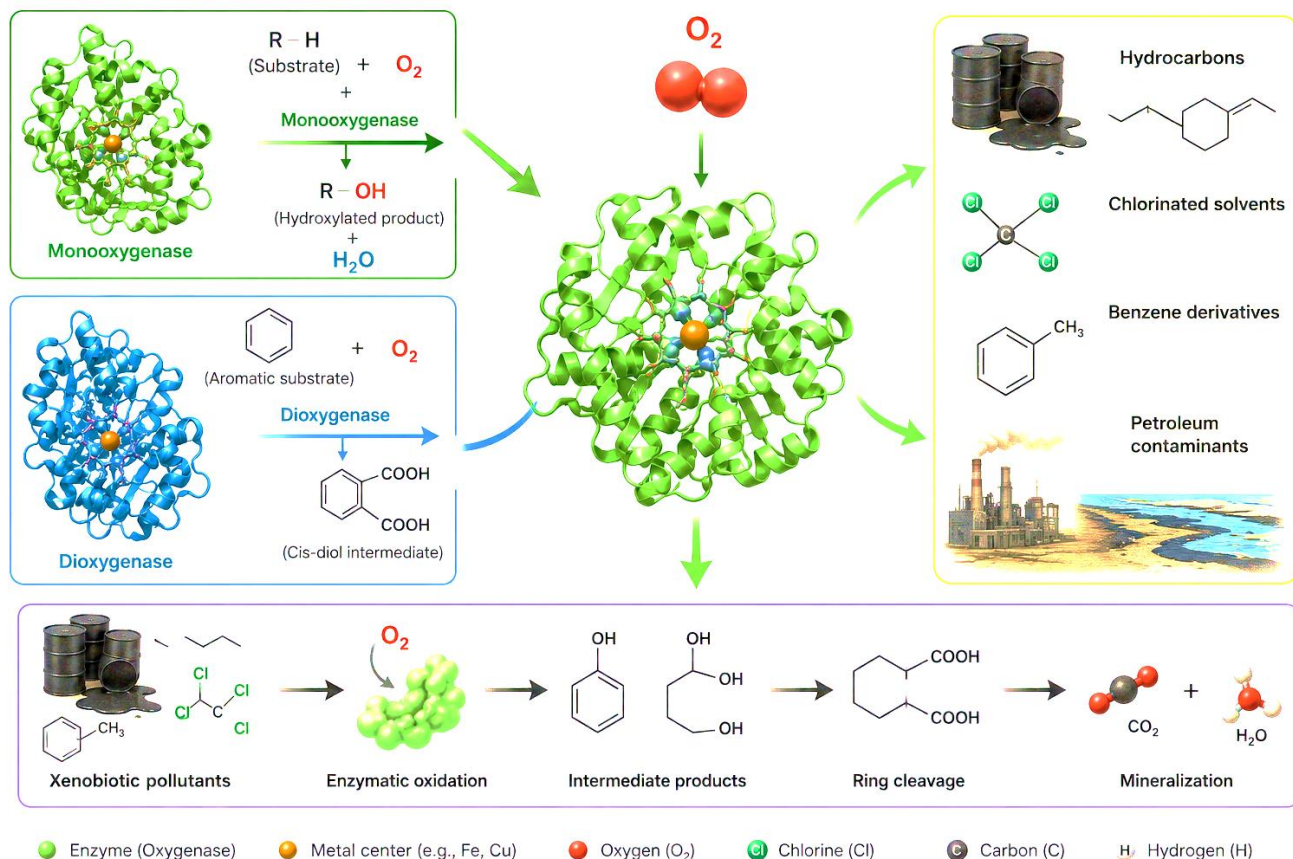


Figure-1. Enzymatic Biodegradation of Xenobiotic Pollutants Mediated by Monooxygenases and Dioxygenases

enzyme discovery has become a central focus of microbial bioprospecting for sustainable remediation technologies.

Among the most important classes of pollutant-degrading enzymes are oxidoreductases, which catalyze electron transfer reactions involved in oxidation or reduction of contaminants. Laccases, multicopper oxidases commonly produced by fungi and some bacteria, are capable of degrading phenolic compounds, synthetic dyes, pharmaceuticals, endocrine disruptors, and lignin-derived pollutants. Their ability to act on structurally diverse aromatic compounds has made them attractive for wastewater treatment and dye decolorization processes (Janusz et al., 2020; Arregui et al., 2019). Similarly, peroxidases such as lignin peroxidase, manganese peroxidase, and versatile peroxidase catalyze oxidative cleavage of complex aromatic molecules in the presence of hydrogen peroxide. These enzymes are particularly effective in degrading recalcitrant dyes, pesticides, and polycyclic aromatic hydrocarbons (Asgher et al., 2020).

Oxygenases also play a crucial role in the biodegradation of xenobiotic pollutants. Monooxygenases incorporate one atom of molecular oxygen into organic substrates, whereas dioxygenases insert two oxygen atoms into aromatic rings, initiating ring cleavage and subsequent mineralization. These enzymes are essential in the degradation of hydrocarbons, chlorinated solvents, benzene derivatives, and petroleum contaminants (Figure-1). Bacterial genera such as *Pseudomonas*, *Rhodococcus*, and *Sphingomonas* are well known for producing oxygenases that attack highly stable hydrocarbon structures (Varjani et al., 2020; Ghosal et al., 2016). Because many industrial pollutants are hydrophobic and chemically inert, oxygenases often represent the first and rate-limiting step in their biodegradation.

Hydrolases constitute another significant group of enzymes involved in pollutant removal. These enzymes catalyze the cleavage of ester, amide, peptide, and glycosidic bonds through the addition of water molecules. Esterases and lipases are widely studied for degradation of pesticides, phthalate esters, and oily waste, while amidases and proteases participate in the transformation of nitrogen-containing pollutants. Cutinases and polyester hydrolases have recently attracted major attention due to their ability to depolymerize synthetic plastics such as polyethylene terephthalate (PET) under mild conditions (Tournier et al., 2020; Wei & Zimmermann, 2017). The emergence of plastic-degrading hydrolases represents a major breakthrough in addressing global plastic pollution.

Transferases and lyases also contribute to pollutant detoxification by modifying chemical groups or breaking molecular bonds without hydrolysis. Glutathione S-transferases, for example, catalyze conjugation reactions that enhance solubility and reduce toxicity of xenobiotic compounds. Dehalogenases are especially important because they remove halogen substituents from chlorinated pesticides, solvents, and industrial chemicals, thereby converting highly toxic molecules into more biodegradable forms (Janssen et al., 2020). These enzymes are valuable for remediating environments contaminated with persistent organohalides.

In many contaminated environments, complete pollutant degradation does not depend on a single enzyme but rather on synergistic enzyme networks. Complex compounds such as crude oil, textile dyes, lignocellulosic residues, or mixed pharmaceutical waste require sequential transformation through multiple oxidative, hydrolytic, and reductive steps. Microbial consortia often outperform individual strains because

different species contribute complementary enzyme systems that collectively achieve full mineralization (Bhatt et al., 2021). This concept has encouraged the design of engineered consortia and immobilized multi-enzyme systems for industrial bioremediation applications.

Recent advances in protein engineering, directed evolution, and computational enzyme design are further enhancing the practical utility of these enzymes. Improvements in thermal stability, catalytic turnover, pH tolerance, and substrate specificity are making novel microbial enzymes increasingly suitable for field-scale remediation. As a result, pollutant-degrading enzymes discovered through microbial bioprospecting are expected to become key components of future green technologies for environmental cleanup

4. Molecular Tools for Enzyme Discovery

The discovery of novel pollutant-degrading enzymes has been significantly accelerated by the development of modern molecular and omics-based technologies. Traditional culture-dependent screening methods, although valuable, are limited by the fact that a vast majority of environmental microorganisms cannot be readily cultivated under laboratory conditions. Consequently, many potentially useful catabolic genes and enzymatic systems remain hidden within uncultured microbial communities. Molecular tools have transformed microbial bioprospecting by enabling direct access to genetic information, functional traits, and metabolic networks from complex environmental samples (Simon & Daniel, 2019; Chistoserdova, 2023). These approaches have greatly expanded the repertoire of enzymes available for environmental biotechnology.

Metagenomics is one of the most powerful strategies for discovering novel enzymes from environmental microbiomes. This approach involves extraction and sequencing of total DNA from habitats such as contaminated soils, marine sediments, wastewater sludge, and landfill sites, followed by bioinformatic analysis of genes encoding catalytic proteins. Metagenomics can be performed through sequence-based screening, where genes are identified through similarity searches, or function-based screening, where cloned environmental DNA libraries are tested for desired enzymatic activities. Through this method, researchers have identified new hydrolases, oxygenases, dehalogenases, laccases, and plastic-degrading enzymes from previously uncultivable microorganisms (Coughlan et al., 2015; Ngara & Zhang, 2018). Because contaminated ecosystems often exert strong selective pressure, metagenomic libraries from these environments are particularly rich in biodegradation-related genes.

Whole-genome sequencing of isolated microbial strains has also become a central tool in enzyme discovery. Sequencing microbial genomes enables the identification of complete catabolic pathways, regulatory genes, transporter systems, and stress-response mechanisms associated with pollutant degradation. Comparative genomics further allows researchers to examine evolutionary adaptations among strains inhabiting contaminated niches (Liu et al., 2022). Genomic analyses of hydrocarbon-degrading bacteria, for instance, have revealed clusters of alkane hydroxylase genes, dioxygenases, biosurfactant synthesis genes, and metal resistance determinants that contribute to efficient bioremediation performance.

Transcriptomics provides insights into gene expression patterns under pollutant stress conditions. By analyzing messenger RNA profiles, researchers can determine which biodegradation genes are actively transcribed in the presence of specific contaminants. This helps distinguish functional genes from silent genes and clarifies regulatory responses during pollutant metabolism. RNA sequencing studies have shown that exposure to dyes, pesticides, and aromatic hydrocarbons can strongly induce oxidoreductases, membrane transporters, and stress adaptation proteins in microbial cells (Su et al., 2021). Such information is valuable for selecting candidate enzymes for industrial application.

Proteomics complements genomics and transcriptomics by identifying proteins that are actually synthesized and functioning within microbial cells or extracellular environments. Since not all transcribed genes are translated into active proteins, proteomic approaches provide more direct evidence of biodegradation mechanisms. Mass spectrometry-based proteomics has been used to characterize extracellular laccases, peroxidases, membrane-bound oxygenases, and hydrolytic enzymes involved in pollutant removal (Borràs et al., 2022). In addition, secretome analysis is particularly important for identifying extracellular enzymes capable of acting directly on insoluble substrates such as plastics, lignin, or oil residues.

Bioinformatics and artificial intelligence have emerged as transformative tools for enzyme mining and optimization. Machine learning algorithms can predict enzyme function, substrate specificity, structural stability, and catalytic efficiency from amino acid sequences. Structural modeling platforms and molecular docking tools help identify active sites and guide rational engineering of enzymes for enhanced degradation performance. AI-assisted screening now enables rapid prioritization of millions of candidate sequences from metagenomic datasets, dramatically reducing time and cost associated with conventional wet-lab discovery (Mazurenko et al., 2020; Jumper et al., 2021).

Another promising development is synthetic biology, where discovered genes are expressed in model hosts such as *Escherichia coli*, *Bacillus subtilis*, or yeast for large-scale enzyme production. Pathway engineering can combine multiple catabolic genes into a single microbial chassis, enabling efficient degradation of mixed pollutants (Keasling, 2021). Such integrated approaches bridge the gap between enzyme discovery and practical environmental deployment. Overall, molecular tools have revolutionized the search for pollutant-degrading enzymes by uncovering hidden microbial potential and enabling precision-based biotechnological development. Continued integration of metagenomics, multi-omics, computational biology, and synthetic biology is expected to deliver next-generation enzymatic solutions for sustainable pollution remediation.

6. Applications In Bioremediation

The discovery of novel microorganisms and pollutant-degrading enzymes through bioprospecting has created substantial opportunities for practical bioremediation. These biological systems are increasingly being applied to contaminated water, soil, industrial waste streams, and emerging pollutant management. Compared with conventional physicochemical treatments, microbial and enzymatic approaches are often more sustainable because they require lower energy input, generate fewer secondary pollutants, and can function under environmentally relevant conditions. As a

result, bioremediation has become an important component of integrated pollution management strategies worldwide (Azubuike et al., 2016; Bilal et al., 2022).

Wastewater treatment is one of the most significant areas where microbial enzymes are being applied. Municipal and industrial wastewaters frequently contain dyes, detergents, pharmaceuticals, endocrine disruptors, hydrocarbons, and heavy metals that are difficult to remove through traditional treatment processes alone. Enzymes such as laccases, peroxidases, and oxygenases have demonstrated strong potential for degrading aromatic compounds, textile dyes, antibiotic residues, and phenolic pollutants in aqueous systems. In biological treatment reactors, microbial consortia can further enhance pollutant removal by combining adsorption, transformation, and mineralization pathways (Arregui et al., 2019; Mulla et al., 2020). Enzyme immobilization on carriers such as biochar, alginate beads, and nanomaterials has also improved catalytic stability and reusability in continuous wastewater treatment systems.

Soil remediation represents another major application of microbial bioprospecting. Agricultural lands, petroleum spill sites, mining areas, and landfill zones are often contaminated with pesticides, hydrocarbons, and toxic metals. Indigenous or introduced microorganisms possessing catabolic enzymes can degrade organic contaminants directly within soil matrices. Hydrocarbon-degrading bacteria, for example, are widely used to remediate oil-contaminated soils through bioaugmentation and biostimulation strategies. Similarly, fungal enzymes such as lignin peroxidase and manganese peroxidase can oxidize persistent pesticide residues and polycyclic aromatic hydrocarbons in soil environments (Varjani et al., 2020; Janusz et al., 2020). In metal-contaminated soils, microbes may contribute through biosorption, bioaccumulation, biomineralization, and redox transformation processes that reduce metal mobility and toxicity.

Industrial effluent treatment has particularly benefited from robust enzymes obtained from extremophilic microorganisms. Effluents generated by textile, paper, petrochemical, tannery, pharmaceutical, and food-processing industries often exhibit high salinity, extreme pH, elevated temperature, and complex contaminant mixtures. Conventional enzymes may lose activity under such harsh conditions, whereas enzymes derived from thermophiles, halophiles, and acidophiles maintain catalytic performance (Coker et al., 2022). Salt-tolerant laccases and thermostable hydrolases have shown promising results in detoxifying colored wastewater, oily sludge, and solvent-rich industrial discharges. These characteristics make extremozymes particularly valuable for industrial-scale environmental biotechnology.

The management of plastic waste and synthetic polymers has emerged as a rapidly expanding field of enzymatic bioremediation. Global plastic accumulation poses severe ecological risks because many polymers resist natural degradation for decades or centuries. Novel enzymes such as PETases, MHETases, cutinases, and polyester hydrolases have demonstrated the ability to depolymerize polyethylene terephthalate and related plastics into reusable monomers under mild conditions. These discoveries have accelerated the concept of circular plastic recycling through enzymatic processing (Tournier et al., 2020; Wei & Zimmermann, 2017). Continued bioprospecting in compost, marine systems, and landfill habitats is expected to reveal additional plastic-degrading enzymes with broader substrate ranges.

Pharmaceutical and personal care product contamination is another emerging challenge where microbial systems offer strong potential. Antibiotics, hormones, analgesics, and cosmetic additives often persist through conventional wastewater treatment and enter rivers or groundwater. Specialized microbial communities enriched from sewage sludge and aquatic sediments have shown the ability to metabolize these compounds through oxidative and hydrolytic pathways (aus der Beek et al., 2016; Gao et al., 2023). Such systems may reduce ecotoxicity and help limit the spread of antimicrobial resistance genes in aquatic environments (Li et al., 2024).

Despite these successes, field-scale applications still require optimization of microbial survival, enzyme stability, mass transfer, and operational economics. Nonetheless, advances in immobilization technologies, bioreactor engineering, synthetic consortia, and gene editing are steadily improving practical performance. Therefore, bioprospected microbial enzymes are increasingly recognized as essential tools for the future of sustainable bioremediation.

7. Challenges and Limitations

Despite the considerable progress achieved in microbial bioprospecting and enzyme-based bioremediation, several scientific, technical, and economic barriers continue to limit widespread implementation. Although laboratory studies frequently demonstrate promising pollutant removal efficiencies, translating these outcomes into consistent field-scale performance remains challenging. Environmental systems are inherently complex, and the success of biological remediation depends on multiple interacting variables including pollutant concentration, nutrient availability, pH, temperature, oxygen status, salinity, competing microorganisms, and contaminant bioavailability (Tyagi et al., 2011; Azubuike et al., 2016). As a result, microorganisms or enzymes that perform efficiently under controlled conditions may show reduced activity in natural settings.

One of the most significant limitations is the low culturability of environmental microorganisms. A large proportion of microbial diversity remains uncultivable using standard laboratory media and incubation conditions. Since many potentially valuable degradative species cannot be grown or maintained in pure culture, their metabolic potential is difficult to validate experimentally. Although metagenomics has helped overcome this obstacle by revealing uncultured genes, expression of environmental genes in surrogate hosts is often inefficient because of codon bias, improper protein folding, lack of cofactors, or incompatible regulatory systems (Steen et al., 2019; Simon & Daniel, 2019). This creates a gap between gene discovery and functional application.

Enzyme instability under operational conditions is another major challenge. Many naturally occurring enzymes lose catalytic activity when exposed to elevated temperature, extreme pH, salinity fluctuations, organic solvents, heavy metals, or prolonged storage. Polluted industrial effluents often contain mixed contaminants that can inhibit enzymatic reactions or denature proteins. Consequently, repeated enzyme supplementation may be required, increasing treatment cost. Although immobilization and protein engineering strategies have improved enzyme robustness, long-term stability under real environmental conditions remains a critical concern (Bilal et al., 2022; Sheldon & Woodley, 2018).

Substrate specificity can also restrict practical utility. Some enzymes exhibit high selectivity toward narrow groups of compounds and therefore may be ineffective against heterogeneous pollutant mixtures commonly found in wastewater, landfill leachate, or contaminated soils. In contrast, broad-spectrum enzymes may generate intermediate metabolites that require additional transformation steps before complete detoxification. This issue is particularly relevant for complex xenobiotics such as pharmaceuticals, chlorinated compounds, and polymeric waste, where multiple enzymes or microbial consortia are needed for total mineralization (Bhatt et al., 2021).

Scale-up and process economics remain important industrial barriers. Large-scale cultivation of microbial strains, purification of enzymes, reactor design, aeration requirements, nutrient supplementation, and downstream monitoring can significantly increase operational expenses. In some cases, conventional physicochemical methods remain faster or more predictable, especially for acute contamination events requiring immediate treatment. Therefore, cost competitiveness is essential for commercial adoption of bioremediation technologies (Rodrigues et al., 2022).

Ecological and biosafety concerns must also be considered. The deliberate release of non-native microorganisms into contaminated environments may disrupt indigenous microbial communities or transfer antibiotic resistance and mobile genetic elements. Similarly, genetically engineered microbes designed for enhanced degradation face regulatory scrutiny regarding containment, persistence, and unintended ecological impacts (de Lorenzo, 2022). Even enzyme-based treatments require assessment of by-products generated during incomplete degradation to ensure that remediation does not create secondary toxicity (Garcia et al., 2023).

Another challenge involves regulatory and policy frameworks. Approval pathways for biological remediation technologies vary substantially among countries and are often slower than those for conventional treatment systems. Lack of standardized protocols for evaluating microbial performance, enzyme efficacy, and environmental safety can delay commercialization and field deployment. In addition, limited awareness among industries and municipalities may hinder investment in biologically based remediation systems.

Data integration and reproducibility also present obstacles in modern bioprospecting. Massive datasets generated from metagenomics, transcriptomics, and proteomics require advanced computational tools and standardized annotation pipelines. Misannotation of genes, insufficient metadata, and lack of publicly accessible validated enzyme databases can slow progress in identifying truly novel biodegradative functions.

Overall, while microbial bioprospecting has opened new frontiers in pollutant remediation, overcoming challenges related to culturability, enzyme stability, scalability, biosafety, and regulation is essential for long-term success. Future progress will depend on interdisciplinary collaboration among microbiologists, engineers, data scientists, policymakers, and industry stakeholders.

8. Future Perspectives

The future of microbial bioprospecting for pollutant degradation is highly promising, particularly as environmental contamination becomes increasingly complex and conventional

remediation approaches face technical and economic limitations. Continued exploration of microbial diversity, combined with rapid advances in biotechnology, is expected to generate more efficient, resilient, and application-ready systems for sustainable environmental management. The next generation of bioremediation strategies will likely move beyond simple organism isolation toward integrated platforms that combine omics technologies, computational modeling, synthetic biology, and process engineering (Nielsen & Keasling, 2016; Chistoserdova, 2023).

One of the most important future directions is the expansion of bioprospecting into underexplored and extreme habitats. Deep-sea sediments, polar ecosystems, desert soils, geothermal springs, hypersaline lakes, acidic mine drainages, and landfill microbiomes are increasingly recognized as reservoirs of unique microorganisms possessing extremozymes with high tolerance to heat, salinity, pH fluctuations, pressure, and toxic chemicals. Such enzymes are particularly valuable for treating industrial effluents and harsh waste streams where conventional catalysts rapidly lose activity (Coker et al., 2022; Elleuche et al., 2015). Continued sampling of these environments is expected to reveal entirely new catalytic mechanisms for degradation of persistent pollutants.

Synthetic biology is likely to transform the practical application of discovered enzymes and microbial pathways. Through genome editing tools such as CRISPR-Cas systems, microbial strains can be engineered for improved pollutant uptake, enhanced metabolic flux, stress resistance, and multi-contaminant degradation capacity. Catabolic genes from different organisms may be assembled into optimized microbial chassis capable of degrading complex waste mixtures more efficiently than natural strains. Similarly, synthetic microbial consortia can be designed to perform sequential degradation steps that mimic ecological cooperation found in nature (Roell et al., 2019; de Lorenzo, 2022; Lunavath et al., 2013; Kumar et al., 2023). These approaches may substantially improve treatment efficiency in wastewater plants, contaminated soils, and industrial reactors.

Protein engineering and directed evolution will continue to improve enzyme performance for environmental applications. Many naturally occurring enzymes possess excellent catalytic functions but limited stability under operational conditions. Rational design, machine learning-guided mutagenesis, and high-throughput screening now allow researchers to enhance thermal resistance, solvent tolerance, catalytic turnover, and substrate specificity (Mazurenko et al., 2020; Arnold, 2018; Porika et al., 2014). In the future, custom-designed enzymes tailored for specific pollutants such as PFAS, microplastics, chlorinated pesticides, or pharmaceutical residues may become feasible (Jumper et al., 2021; Janakiramulu et al., 2025).

Artificial intelligence and advanced bioinformatics are expected to play an increasingly central role in enzyme mining. Massive genomic and metagenomic databases contain millions of uncharacterized sequences, many of which likely encode useful degradative proteins. AI models can rapidly predict enzyme structure, active sites, catalytic function, and environmental suitability, thereby reducing the time required for experimental screening (Jumper et al., 2021; Thornton et al., 2022; Namthabhad et al., 2014; Swapna et al., 2024). Integration of machine learning with robotics and automated laboratories may enable fully accelerated discovery pipelines for novel biodegradation catalysts.

Immobilization technologies and smart bioreactor systems also represent major future opportunities. Enzymes immobilized on nanomaterials, biochar, membranes, hydrogels, or magnetic particles can achieve higher stability, easier recovery, and repeated reuse. Coupling these systems with real-time sensors, digital monitoring, and automated process control may optimize pollutant removal efficiency while lowering operational cost. Such innovations are especially relevant for decentralized wastewater treatment and industrial effluent management.

Another critical future direction is the integration of bioremediation into the circular bioeconomy. Instead of viewing pollutants solely as waste, future technologies may recover value-added products during biodegradation processes. For example, plastic depolymerization can generate recyclable monomers, hydrocarbon waste can be converted into biosurfactants or bioplastics, and nutrient-rich wastewater can support biomass production (Tournier et al., 2020; Stegmann et al., 2020). This resource recovery perspective can improve economic feasibility and sustainability simultaneously.

Despite these opportunities, responsible innovation will remain essential. Biosafety regulations, ecological risk assessment, public acceptance, and ethical considerations surrounding engineered microbes must accompany technological progress. International collaboration, open-access genomic databases, and multidisciplinary partnerships will be crucial for translating laboratory discoveries into field-ready solutions.

Overall, the future of microbial bioprospecting lies in combining natural biodiversity with advanced engineering tools. Such integration has the potential to revolutionize pollutant remediation and contribute significantly to global environmental sustainability.

9. Conclusion

Environmental pollution continues to pose a major threat to ecosystem integrity, biodiversity conservation, and human health across the globe. The persistent release of hydrocarbons, pesticides, dyes, pharmaceuticals, plastics, and heavy metals into natural environments has intensified the need for efficient and sustainable remediation strategies. Although conventional physicochemical methods remain useful in specific contexts, their limitations such as high cost, incomplete treatment efficiency, and secondary waste generation have encouraged the search for greener alternatives.

In this regard, microbial bioprospecting has emerged as a highly valuable approach for discovering novel microorganisms and enzymatic systems capable of degrading diverse environmental pollutants. Microbial communities inhabiting contaminated and extreme environments possess unique adaptive metabolisms that enable transformation of recalcitrant compounds into less toxic products. Enzymes such as oxidoreductases, hydrolases, oxygenases, and depolymerases have demonstrated substantial potential in the remediation of wastewater, contaminated soils, industrial effluents, and plastic waste.

Recent progress in metagenomics, multi-omics technologies, bioinformatics, artificial intelligence, and synthetic biology has significantly expanded access to previously unexplored microbial resources. These advances are accelerating the identification, optimization, and large-scale

application of efficient biodegradative enzymes. At the same time, innovations in immobilization techniques, engineered microbial consortia, and smart bioprocess systems are improving operational stability and commercial feasibility. Despite these developments, several challenges remain, including enzyme stability under environmental conditions, scale-up constraints, regulatory approval processes, and biosafety considerations. Addressing these limitations through interdisciplinary collaboration and translational research will be essential for broader implementation.

Overall, microbial bioprospecting represents a transformative pathway toward sustainable environmental management. Continued exploration of microbial diversity, coupled with advanced biotechnological innovation, has the potential to revolutionize pollutant remediation and support the global transition toward a cleaner, safer, and circular bioeconomy.

Competing interests:

The authors declare that they have no competing interests

References

- [1] Ali, S. S., Al-Tohamy, R., Koutra, E., Moawad, M. S., Kornaros, M., Mustafa, A. M., & Sun, J. (2021). Plastic wastes biodegradation: Mechanisms, challenges and future prospects. *Science of the Total Environment*, 780, 146590.
- [2] Almeida, E. L., Silva, R. N., & Souza, D. T. (2023). Microbial diversity as a source of novel industrial enzymes: Advances in environmental bioprospecting. *Biotechnology Advances*, 67, 108192.
- [3] Arnold, F. H. (2018). Directed evolution: Bringing new chemistry to life. *Angewandte Chemie International Edition*, 57(16), 4143–4148.
- [4] Arregui, L., Ayala, M., Gómez-Gil, X., Gutiérrez-Soto, G., Hernández-Luna, C. E., Herrera de Los Santos, M., & Levin, L. (2019). Laccases: Structure, function, and potential application in water bioremediation. *Microbial Cell Factories*, 18, 200.
- [5] Asgher, M., Noreen, S., Bilal, M., & Asgher, Z. (2020). Enhancement of ligninolytic enzyme production and their biotechnological applications. *Biocatalysis and Agricultural Biotechnology*, 25, 101569.
- [6] aus der Beek, T., Weber, F.-A., Bergmann, A., Hickmann, S., Ebert, I., Hein, A., & Küster, A. (2016). Pharmaceuticals in the environment—Global occurrences and perspectives. *Environmental Toxicology and Chemistry*, 35(4), 823–835.
- [7] Azubuike, C. C., Chikere, C. B., & Okpokwasili, G. C. (2016). Bioremediation techniques—Classification based on site of application: Principles, advantages, limitations and prospects. *World Journal of Microbiology and Biotechnology*, 32, 180.
- [8] Bhatt, P., Bhandari, G., Sharma, A., Zhang, W., Zhao, Q., & Chen, S. (2021). Biotechnological basis of microbial degradation of pesticides in contaminated environments. *Critical Reviews in Biotechnology*, 41(3), 317–340.
- [9] Bilal, M., Iqbal, H. M. N., Barceló, D., & Wang, J. (2022). Enzymatic degradation of environmental pollutants: Mechanisms and recent advances. *Chemosphere*, 307, 135941.
- [10] Borràs, E., Ferrer, C., Llorca, C., & Caminal, G. (2022). Proteomics approaches for discovering enzymes involved in environmental biodegradation processes. *Journal of Proteomics*, 252, 104418.
- [11] Chistoserdova, L. (2023). Functional metagenomics and uncultivated microbes in environmental biotechnology. *Current Opinion in Biotechnology*, 79, 102859.
- [12] Coker, J. A., Bowers, K. J., & Shams, M. (2022). Extremophiles and extremozymes for industrial and environmental

- biotechnology. *Current Opinion in Biotechnology*, 73, 129–136.
- [13] Coughlan, L. M., Cotter, P. D., Hill, C., & Alvarez-Ordóñez, A. (2015). New weapons to fight old enemies: Novel strategies for the discovery of antibacterial enzymes from metagenomes. *Frontiers in Microbiology*, 6, 1298.
 - [14] de Lorenzo, V. (2022). Environmental biosafety of engineered microorganisms for biotechnology applications. *Current Opinion in Biotechnology*, 74, 184–191.
 - [15] Elleuche, S., Schröder, C., Sahm, K., & Antranikian, G. (2015). Extremozymes—Biocatalysts with unique properties from extremophilic microorganisms. *Current Opinion in Biotechnology*, 29, 116–123.
 - [16] Gao, Y., Chen, J., Liu, X., Wang, H., & Zhao, L. (2023). Occurrence, fate, and ecological risks of pharmaceutical and personal care products in aquatic environments: A global review. *Journal of Hazardous Materials*, 452, 131265.
 - [17] Garcia, M. R., Santos, P. L., Oliveira, J. A., & Costa, R. F. (2023). Toxic by-products generated during incomplete biodegradation: Environmental risk assessment and mitigation strategies. *Environmental Research*, 233, 116512.
 - [18] Ghosal, D., Ghosh, S., Dutta, T. K., & Ahn, Y. (2016). Current state of knowledge in microbial degradation of polycyclic aromatic hydrocarbons. *Frontiers in Microbiology*, 7, 1369.
 - [19] Janssen, D. B., Dinkla, I. J. T., Poelarends, G. J., & Terpstra, P. (2020). Bacterial dehalogenation enzymes and their applications. *Current Opinion in Biotechnology*, 62, 1–8.
 - [20] Janusz, G., Pawlik, A., Świdarska-Burek, U., Polak, J., Sulej, J., Jarosz-Wilkolazka, A., & Paszczyński, A. (2020). Laccase properties, physiological functions, and evolution. *International Journal of Molecular Sciences*, 21(3), 966.
 - [21] Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., ... & Hassabis, D. (2021). Highly accurate protein structure prediction with AlphaFold. *Nature*, 596, 583–589.
 - [22] Keasling, J. D. (2021). Synthetic biology and the development of tools for metabolic engineering. *Metabolic Engineering*, 65, 1–2.
 - [23] Kumar, R., Sharma, P., Verma, A., & Singh, D. (2021). Environmental persistence and ecological risks of industrial organic pollutants: Sources, pathways, and remediation strategies. *Environmental Pollution*, 286, 117489.
 - [24] Li, M., Zhou, Q., Wu, Y., Song, Y., & Wang, C. (2022). Heavy metal contamination in soils and crops: Sources, transfer mechanisms, and human health implications. *Science of the Total Environment*, 825, 153862.
 - [25] Li, X., Wang, T., Zhou, J., & Chen, H. (2024). Pharmaceutical pollutants and antimicrobial resistance risks in aquatic ecosystems: Microbial mitigation approaches. *Journal of Hazardous Materials*, 461, 132401.
 - [26] Liu, X., Zhang, Y., Chen, H., & Wang, J. (2022). Comparative genomics reveals catabolic pathways and adaptive evolution in pollutant-degrading bacteria. *Science of the Total Environment*, 824, 153824.
 - [27] Mazurenko, S., Prokop, Z., & Damborsky, J. (2020). Machine learning in enzyme engineering. *ACS Catalysis*, 10(2), 1210–1223.
 - [28] Mulla, S. I., Bharagava, R. N., & Saratale, G. D. (2020). Microbial consortia for removal of dyes and emerging pollutants from wastewater: Current advances and future prospects. *Bioresource Technology*, 307, 123233.
 - [29] Mulligan, C. N. (2021). Environmental applications for biosurfactants in soil and water remediation. *Current Opinion in Environmental Science & Health*, 20, 100237.
 - [30] Ngara, T. R., & Zhang, H. (2018). Recent advances in function-based metagenomic screening. *Genomics, Proteomics & Bioinformatics*, 16(6), 405–415.
 - [31] Nielsen, J., & Keasling, J. D. (2016). Engineering cellular metabolism. *Cell*, 164(6), 1185–1197.
 - [32] Rodrigues, A. C., Silva, M. R., & Mendes, R. (2022). Techno-economic challenges in scaling up industrial bioremediation systems. *Journal of Cleaner Production*, 360, 132104.
 - [33] Roell, G. W., Zha, J., Carr, R. R., Koffas, M. A. G., Fong, S. S., & Tang, Y. J. (2019). Engineering microbial consortia by division of labor. *Microbial Cell Factories*, 18, 35.
 - [34] Saravanan, A., Kumar, P. S., Jeevanantham, S., Karishma, S., Yaashikaa, P. R., & Reshma, B. (2022). Effective water/wastewater treatment methodologies for toxic pollutants removal: Processes and applications toward sustainability. *Chemosphere*, 280, 130595.
 - [35] Sharma, A., Bhatt, P., Zhao, Q., & Chen, S. (2023). Emerging microbial enzymes for biodegradation of recalcitrant environmental pollutants. *Journal of Hazardous Materials*, 451, 131156.
 - [36] Sheldon, R. A., & Woodley, J. M. (2018). Role of biocatalysis in sustainable chemistry. *Chemical Reviews*, 118(2), 801–838.
 - [37] Simon, C., & Daniel, R. (2019). Metagenomic analyses: Past and future trends. *Applied and Environmental Microbiology*, 85(3), e02226-18.
 - [38] Singh, R., Kumar, A., Patel, S., & Verma, N. (2024). Ecological disruption caused by persistent contaminants: Impacts on soil fertility and aquatic biodiversity. *Science of the Total Environment*, 906, 167845.
 - [39] Steen, A. D., Crits-Christoph, A., Carini, P., DeAngelis, K. M., Fierer, N., Lloyd, K. G., & Thrash, J. C. (2019). High proportions of bacteria and archaea across most biomes remain uncultured. *The ISME Journal*, 13, 3126–3130.
 - [40] Stegmann, P., Londo, M., & Junginger, M. (2020). The circular bioeconomy: Its elements and role in European bioeconomy clusters. *Resources, Conservation and Recycling*, 153, 104553.
 - [41] Su, J., Zhang, Q., Li, M., & Li, X. (2021). Transcriptomic responses of pollutant-degrading microorganisms under xenobiotic stress conditions. *Environmental Research*, 197, 111132.
 - [42] Tchounwou, P. B., Yedjou, C. G., Patlolla, A. K., & Sutton, D. J. (2012). Heavy metal toxicity and the environment. *EXS*, 101, 133–164.
 - [43] Thornton, J. M., Laskowski, R. A., & Borkakoti, N. (2022). Computational prediction of enzyme function in the era of big biological data. *Nature Reviews Methods Primers*, 2, 25.
 - [44] Tournier, V., Topham, C. M., Gilles, A., David, B., Folgoas, C., Moya-Leclair, E., ... & Marty, A. (2020). An engineered PET depolymerase to break down and recycle plastic bottles. *Nature*, 580, 216–219.
 - [45] Trincone, A. (2022). Marine biocatalysts and enzymes for environmental and industrial applications. *Marine Drugs*, 20(5), 315.
 - [46] Tyagi, M., da Fonseca, M. M. R., & de Carvalho, C. C. C. R. (2011). Bioaugmentation and biostimulation strategies to improve the effectiveness of bioremediation processes. *Biodegradation*, 22, 231–241.
 - [47] Varjani, S., Upasani, V. N., & Pandey, A. (2020). Bioremediation of petroleum hydrocarbons by microbial systems: Current progress and future prospects. *Bioresource Technology*, 300, 122730.
 - [48] Wang, T., He, J., Liu, Z., & Zhang, Y. (2023). Global trends in environmental contamination and ecosystem responses under anthropogenic pressure. *Environmental Research*, 225, 115611.
 - [49] Wei, R., & Zimmermann, W. (2017). Microbial enzymes for the recycling of recalcitrant petroleum-based plastics. *Microbial Biotechnology*, 10(6), 1308–1322.
 - [50] Zhang, L., Xu, H., Chen, S., & Huang, J. (2024). Persistent organic pollutants in soil and water systems: Distribution, toxicity, and remediation opportunities. *Chemosphere*, 355, 141923.
 - [51] Janakiramulu, P., & Mamidala, E. (2025). Molecular Docking and dynamic simulation analysis of flavonoid derivatives as COX-2 inhibitors. *In Silico Pharmacology*, 13(2), 59.

- [52] Namthabad, S., & Mamidala, E. (2014). Molecular docking of HIV-1 protease using alkaloids from *tinospora cordifolia*. *Int J Res Appl*, 1(1), 12-6.
- [53] Swapna, K., Srujana, M., & Mamidala, E. (2024). Identification of steroidal cardenolides from *Calotropis procera* as novel HIV-1 PR inhibitors: A molecular docking & molecular dynamics simulation study. *The Indian journal of medical research*, 160(1), 78.
- [54] Lunavath, V., & Mamidala, E. (2013). Preliminary phytochemical screening and antibacterial studies of the leaves of *Eclipta alba* (L). *Int J Pharma Biosci*, 4, 380-4.
- [55] Kumar, M. P., Mamidala, E., Al-Ghanim, K., Al-Misned, F., Ahmed, Z., & Mahboob, S. (2020). Effects of D-Limonene on aldose reductase and protein glycation in diabetic rats. *Journal of King Saud University-Science*, 32(3), 1953-1958.
- [56] Porika, R., Poojari, S., Lunavath, V., & Mamidala, E. (2014). Preliminary phytochemical investigation and TLC analysis of *P. angulata* fruit extract. *Journal of Pharmacy and Biological Sciences*, 9(2), 11-14.

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